In the Claims

Please cancel claims 16 and 36 without prejudice.

Please amend claims 17, 20, 22, 23, 42, 45 and 48 as follows:

Claims 1-16. (Cancelled)

17. (Currently Amended) The method of claim ~~16~~ 48, wherein at least one of the interacting molecules contains a DNA-binding moiety and at least one of the interacting molecules contains a transcriptional activation or a transcriptional repressor moiety.

18. (Original) The method of claim 17, wherein the DNA-binding moiety and the transcriptional activation moiety are derived from a single transcriptional activator.

19. (Original) The method of claim 17, wherein the DNA-binding moiety and the transcriptional activation moiety are derived from different proteins.

20. (Currently Amended) The method of claim ~~16~~ 48, wherein the detectable signal is produced from a gene encoding a protein selected from the group consisting of β-galactosidase, green fluorescent protein. luciferase, alkaline phosphatase and chloramphenicol acetyl transferase.

22. (Currently Amended) The method of claim ~~16~~ 48, wherein the detectable signal is encoded by a gene present in the host cell.

23. (Currently Amended) The method of claim 22, wherein the host cell further comprises a first recombinant gene encoding the first molecule, a second recombinant gene encoding the second molecule, or a third recombinant gene encoding the third molecule[,].

24. (Previously Presented) The method of claim 23, wherein the host cell contains both the first gene and the second gene and each gene is expressed.

25. (Previously Presented) The method of claim 23, wherein the host cell contains the first, second and third genes and each gene is expressed.

Claims 26-41. (Cancelled)

42. (Currently Amended) The method of claim ~~36~~ 48, wherein the third molecule contains a DNA binding domain and a transcriptional activation domain.

Claims 43-44 (Cancelled)

45. (Currently Amended) The method of claim ~~36~~ 48, further comprising, prior to step (i):

obtaining the mixed population of organisms from an environmental sample; and

enriching the sample for prokaryotic organisms, thereby creating an enriched environmental sample, wherein said sample is used to generate the library.

46. (Previously Presented) The method of claim 45, further comprising producing a normalized library, comprising :

isolating nucleic acids from said enriched environmental sample;

fractionating the isolated nucleic acids; and

amplifying any single-stranded nucleic acids present in the same cell.

47. (Previously Presented) The method of claim 46, further comprising generating an expression library, comprising:

inserting the amplified and isolated nucleic acids into an expression vector.

48. (Currently Amended) A method for screening for the presence of a molecule that affects the interaction between a first and second molecule, comprising:

(i) contacting in a cell a first molecule with a second molecule wherein at least one of the first or second molecules is derived from a library made from a mixed population of organisms, wherein association of the first and second molecules in the presence of a third molecule results in the presence of a detectable response by changing expression of a detectable gene or detectable gene product; and

(ii) comparing the detectable response in the presence of the third molecule and the first and second molecules with the detectable response in the absence of the third molecule, wherein a difference in response is indicative of [[a]] first and second molecules that interact and a third molecule that affects the interaction between the first and second molecules, thereby identifying the presence of a molecule that affects the interaction of the first and second molecules.

49. (Previously Added) The method of claim 48, wherein a nucleic acid sequence encoding the third molecule is determined.

Please add the following new claim:

50. (New) The method of claim 48, wherein the third molecule is derived from the mixed population of organisms.